

Amendment to the Claims:

Please amend the claims as follows.

Please cancel claims 6 to 8, without prejudice.

This listing of claims will replace all prior versions, and listing, of claims in the application:

Listing of Claims:

Claim 1 (currently amended): A computer readable medium having stored thereon a nucleic acid sequence having at least 70% sequence identity to a region of at least about 100 residues of a sequence as set forth in SEQ ID NO:1, and sequences substantially identical thereto, or a nucleic acid sequence encoding a polypeptide sequence having at least 70% sequence identity to a region of at least about 100 residues of a sequence as set forth in SEQ ID NO:2, and sequences substantially identical thereto, wherein the computer readable medium can receive instructions for causing a computer to determine differences between the nucleic acid sequence and a reference sequence or identify a feature in the nucleic acid sequence.

Claim 2 (currently amended): A computer system comprising a processor and a data storage device wherein said data storage device has stored thereon a nucleic acid sequence having at least 70% sequence identity to a region of at least about 100 residues of a sequence as set forth in SEQ ID NO:1, and sequences substantially identical thereto, or a nucleic acid sequence encoding a polypeptide sequence having at least 70% sequence identity to a region of at least about 100 residues of a sequence as set forth in SEQ ID NO:2, and sequences substantially identical thereto and instructions for causing a computer to determine differences between the nucleic acid sequence and a reference sequence or identify a feature in the nucleic acid sequence.

Claim 3 (original): The computer system of claim 1, further comprising a sequence comparison algorithm and a data storage device having at least one reference sequence stored thereon.

Claim 4 (original): The computer system of claim 2, wherein the sequence comparison algorithm comprises a computer program which indicates polymorphisms.

Claim 5 (original): The computer system of claim 1, further comprising an identifier which identifies features in said sequence.

Claims 6 to 8 (canceled)

Claim 9 (new): A computer readable medium having stored thereon a plurality of instructions comprising an instruction which, when executed by a processor, causes the processor to implement a method of comparing at least two nucleic acid sequences, wherein one nucleic acid sequence has at least 70% sequence identity to a region of at least about 100 residues of SEQ ID NO:1, or comprises a sequence encoding a polypeptide having at least 70% sequence identity to a region of at least about 100 residues of SEQ ID NO:2.

Claim 10 (new): A computer readable medium having stored thereon a plurality of instructions comprising an instruction which, when executed by a processor, causes the processor to implement a method of identifying a feature in a nucleic acid sequence, wherein the nucleic acid sequence comprises a sequence having at least 70% sequence identity to a region of at least about 100 residues of SEQ ID NO:1, or comprising a sequence encoding a polypeptide having at least 70% sequence identity to a region of at least about 100 residues of SEQ ID NO:2.

Claim 11 (new): A computer program product that can determine differences between a nucleic acid sequence and a reference sequence or identify a feature in a nucleic acid sequence, comprising

a computer code that can determine differences between a nucleic acid sequence and a reference sequence or identify a feature in a nucleic acid sequence, comprising a sequence having at least 70% sequence identity to a region of at least about 100 residues of SEQ ID NO:1, or comprising a sequence encoding a polypeptide having at least 70% sequence identity to a region of at least about 100 residues of SEQ ID NO:2; and

a computer readable medium that stores the computer code.

Claim 12 (new): A computer system comprising a processor and a computer program product as set forth in claim 11.

Claim 13 (new): A computer program, stored on a computer-readable medium, for determining differences between a nucleic acid sequence and a reference sequence or identifying a feature in a nucleic acid sequence, comprising instructions for determining differences between a nucleic acid sequence and a reference sequence or identifying a feature in a nucleic acid sequence, and comprising a sequence having at least 70% sequence identity to a region of at least about 100 residues of SEQ ID NO:1, or comprising a sequence encoding a polypeptide having at least 70% sequence identity to a region of at least about 100 residues of SEQ ID NO:2.

Claim 14 (new): A computer-readable medium having computer-executable instructions for performing a method comprising determining differences between a nucleic acid sequence and a reference sequence or identifying a feature in a nucleic acid sequence, and comprising a sequence having at least 70% sequence identity to a region of at least about 100 residues of SEQ ID NO:1, or comprising a sequence encoding a polypeptide having at least 70% sequence identity to a region of at least about 100 residues of SEQ ID NO:2.

Claim 15 (new): The computer readable medium of claim 1 or claim 14, wherein the nucleic acid has at least 80% sequence identity to SEQ ID NO:1 or encodes a polypeptide having at least 80% sequence identity to SEQ ID NO:2.

Claim 16 (new): The computer readable medium of claim 15, wherein the nucleic acid has at least 90% sequence identity to SEQ ID NO:1 or encodes a polypeptide having at least 90% sequence identity to SEQ ID NO:2.

Claim 17 (new): The computer readable medium of claim 16, wherein the nucleic acid has at least 95% sequence identity to SEQ ID NO:1 or encodes a polypeptide having at least 95% sequence identity to SEQ ID NO:2.

Claim 18 (new): The computer readable medium of claim 17, wherein the nucleic acid has a sequence as set forth in SEQ ID NO:1 or encodes a polypeptide having a sequence as set forth in SEQ ID NO:2.

Claim 19 (new): The computer readable medium of claim 1 or claim 14, wherein the nucleic acid has a sequence identity to SEQ ID NO:1 over region of at least about 150 residues or the polypeptide has a sequence identity to SEQ ID NO:2 over region of at least about 150 residues.

Claim 20 (new): The computer readable medium of claim 19, wherein the nucleic acid has a sequence identity to SEQ ID NO:1 over region of at least about 200 residues or the polypeptide has a sequence identity to SEQ ID NO:2 over region of at least about 200 residues.

Claim 21 (new): The computer readable medium of claim 20, wherein the nucleic acid has a sequence identity to SEQ ID NO:1 over region of at least about 300 residues or the polypeptide has a sequence identity to SEQ ID NO:2 over region of at least about 300 residues.

Claim 22 (new): The computer readable medium of claim 21, wherein the nucleic acid has a sequence identity to SEQ ID NO:1 over region of at least about 400 residues or the polypeptide has a sequence identity to SEQ ID NO:2 over region of at least about 400 residues.

Claim 23 (new): The computer readable medium of claim 22, wherein the nucleic acid has a sequence identity to SEQ ID NO:1 over the entire length of the sequence or the polypeptide has a sequence identity to SEQ ID NO:2 over the entire length of the sequence.